

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,841

DATE: 10/30/2001

TIME: 12:42:28

Input Set : A:\2577-109.app

Output Set: N:\CRF3\10302001\I857841.raw

ENTERED

3 <110> APPLICANT: Fang, Rong-Xiang
4 Wu, Jun-Lin
5 Chen, Xiao-Ying
7 <120> TITLE OF INVENTION: ENHANCED PROTEIN PRODUCTION IN HIGHER PLANTS BY
8 N-TERMINAL FUSION OF A UBIQUITIN OR A CUCUMBER MOSAIC
9 VIRUS COAT PROTEIN PEPTIDE
11 <130> FILE REFERENCE: 2577-109
13 <140> CURRENT APPLICATION NUMBER: 09/857,841
C--> 14 <141> CURRENT FILING DATE: 1998-12-11
16 <150> PRIOR APPLICATION NUMBER: PCT/SG98/00103
17 <151> PRIOR FILING DATE: 1998-12-11
19 <160> NUMBER OF SEQ ID NOS: 14
21 <170> SOFTWARE: PatentIn Ver. 2.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 235
25 <212> TYPE: DNA
26 <213> ORGANISM: Nicotiana tabacum
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (3)..(230)
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Modified from wild-type to insert an SphI site in
34 the region encompassing the initiation codon ATG
35 and to insert an NcoI site following the last
36 codon GGC.
38 <400> SEQUENCE: 1
39 gc atg cag atc ttc gta aag acc ctg acg ggg aag act att acc tta 47
40 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu
41 1 5 10 15
43 gag gta gag tca tcg gac acc att gac aat gtt aag gct aag att cag 95
44 Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln
45 20 25 30
47 gac aag gaa ggc att cca ccg gac cag cag cgg ttg att ttc gca ggt 143
48 Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly
49 35 40 45
51 aag cag ctt gag gat ggc cga aca cta gct gac tac aac atc cag aag 191
52 Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys
53 50 55 60
55 gag tcc act ctc cat ctc gtc tta aga ctc cgc ggt ggc catgg 235
56 Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
57 65 70 75
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 76
62 <212> TYPE: PRT
63 <213> ORGANISM: Nicotiana tabacum
65 <400> SEQUENCE: 2
66 Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu

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67   1           5           10           15
69 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
70           20           25           30
72 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
73           35           40           45
75 Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
76           50           55           60
78 Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
79 65           70           75
82 <210> SEQ ID NO: 3
83 <211> LENGTH: 53
84 <212> TYPE: DNA
85 <213> ORGANISM: cucumber mosaic virus
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (6)..(47)
91 <400> SEQUENCE: 3
92 gatcc atg gac aaa tct gaa tca acc agt gct ggt cgt aac cgt cga 47
93 Met Asp Lys Ser Glu Ser Thr Ser Ala Gly Arg Asn Arg Arg
94   1           5           10
96 cgagct 53
99 <210> SEQ ID NO: 4
100 <211> LENGTH: 14
101 <212> TYPE: PRT
102 <213> ORGANISM: cucumber mosaic virus
104 <400> SEQUENCE: 4
105 Met Asp Lys Ser Glu Ser Thr Ser Ala Gly Arg Asn Arg Arg
106 1           5           10
109 <210> SEQ ID NO: 5
110 <211> LENGTH: 13
111 <212> TYPE: DNA
112 <213> ORGANISM: Plasmid pSKUBC1
114 <220> FEATURE:
115 <221> NAME/KEY: misc_feature
116 <222> LOCATION: ( ).. )
117 <223> OTHER INFORMATION: Joining region of fusion of two genes.
119 <400> SEQUENCE: 5
120 ggccatggac aaa 13
123 <210> SEQ ID NO: 6
124 <211> LENGTH: 33
125 <212> TYPE: DNA
126 <213> ORGANISM: Plasmid pBI221
128 <220> FEATURE:
129 <221> NAME/KEY: misc_feature
130 <222> LOCATION: (1)..(33)
131 <223> OTHER INFORMATION: Joining region between 35S promoter and GUS gene.
133 <400> SEQUENCE: 6
134 tctagaggat ccccggtgg tcagtcctt atg 33
137 <210> SEQ ID NO: 7

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138 <211> LENGTH: 18
139 <212> TYPE: DNA
140 <213> ORGANISM: Plasmid pUG
142 <220> FEATURE:
143 <221> NAME/KEY: misc_feature
144 <222> LOCATION: (1)..(18)
145 <223> OTHER INFORMATION: Joining region of fusion of genes.
147 <400> SEQUENCE: 7
148 ggccatggat ccccggtt                                     18
151 <210> SEQ ID NO: 8
152 <211> LENGTH: 18
153 <212> TYPE: DNA
154 <213> ORGANISM: Plasmid pUCG2
156 <220> FEATURE:
157 <221> NAME/KEY: misc_feature
158 <222> LOCATION: (1)..(18)
159 <223> OTHER INFORMATION: Joining region of fusion of genes.
161 <400> SEQUENCE: 8
162 ctccgcggtg gcatggac                                     18
165 <210> SEQ ID NO: 9
166 <211> LENGTH: 29
167 <212> TYPE: DNA
168 <213> ORGANISM: Plasmid pBIubi
170 <220> FEATURE:
171 <221> NAME/KEY: misc_feature
172 <222> LOCATION: (1)..(29)
173 <223> OTHER INFORMATION: Joining region between promoter and fused gene.
175 <400> SEQUENCE: 9
176 tctagaacta gtggatccct ggcatgcg                         29
179 <210> SEQ ID NO: 10
180 <211> LENGTH: 35
181 <212> TYPE: DNA
182 <213> ORGANISM: Plasmid pBIubi
184 <220> FEATURE:
185 <221> NAME/KEY: misc_feature
186 <222> LOCATION: (1)..(35)
187 <223> OTHER INFORMATION: Final 2 codons of the ubiquitin gene followed by
188     polylinker sequence.
190 <400> SEQUENCE: 10
191 ggaggcctgt cgactcgagc ccgggtaccg agctc                 35
194 <210> SEQ ID NO: 11
195 <211> LENGTH: 12
196 <212> TYPE: DNA
197 <213> ORGANISM: Plasmid pUL
199 <220> FEATURE:
200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: (1)..(12)
202 <223> OTHER INFORMATION: Joining region between fusion of genes.
204 <400> SEQUENCE: 11

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205 ggagggcatgg aa 12
208 <210> SEQ ID NO: 12
209 <211> LENGTH: 12
210 <212> TYPE: DNA
211 <213> ORGANISM: Plasmid pCL
213 <220> FEATURE:
214 <221> NAME/KEY: misc_feature
215 <222> LOCATION: (1)..(12)
216 <223> OTHER INFORMATION: Joining region between fusion of genes.
218 <400> SEQUENCE: 12
219 cgtcgcatgg aa 12
222 <210> SEQ ID NO: 13
223 <211> LENGTH: 29
224 <212> TYPE: DNA
225 <213> ORGANISM: Plasmid pBIubi
227 <220> FEATURE:
228 <221> NAME/KEY: misc_feature
229 <222> LOCATION: (1)..(29)
230 <223> OTHER INFORMATION: Joining region of fusion of promoter and gene.
232 <400> SEQUENCE: 13
233 tctagaacta gtggatccct ggcattgag 29
236 <210> SEQ ID NO: 14
237 <211> LENGTH: 35
238 <212> TYPE: DNA
239 <213> ORGANISM: Plasmid pBIubi
241 <220> FEATURE:
242 <221> NAME/KEY: misc_feature
243 <222> LOCATION: (1)..(35)
244 <223> OTHER INFORMATION: Joining region with multicloning sequence between
245 fusion of gene and terminator.
247 <400> SEQUENCE: 14
248 ggaggcctgt cgactcgagc ccgggtaccg agctc 35

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VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date